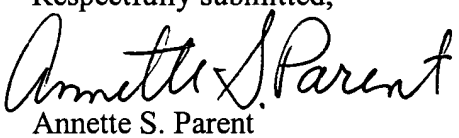
Attached hereto is a marked-up version of the changes made to the Specification and Claims by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."** As a convenience to the Examiner, a complete set of the Claims, as amended herein, is also attached to this Amendment as an appendix entitled **"PENDING CLAIMS WITH ENTRY OF THE AMENDMENT"**.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 22 of page 15 has been amended as follows:

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., comprising a sequence of or encoded by ~~nucleotide sequences~~ SEQ ID NO:1-25), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

In the Claims:

Please amend claim 33 as follows:

33. (Once Amended) The method of claim 25, wherein the T1R2 polypeptide has an amino acid sequence of SEQ ID NO:7, 8, or 9 ~~SEQ ID NO:6, 7, or 8~~.

PENDING CLAIMS WITH ENTRY OF THE AMENDMENT

1. (As filed) An isolated sweet taste receptor comprising a T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25.

2. (As filed) The isolated receptor of claim 1, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25.

3. (As filed) The isolated receptor of claim 1, wherein the T1R3 polypeptide has an amino acid sequence of SEQ ID NO:15, 20, 23, or 25.

4. (As filed) The isolated receptor of claim 1, wherein the receptor comprises a T1R3 polypeptide and a heterologous polypeptide.

5. (As filed) The isolated receptor of claim 4, wherein the T1R3 polypeptide and the heterologous polypeptide are non-covalently linked.

6. (As filed) The isolated receptor of claim 4, wherein the T1R3 polypeptide and the heterologous polypeptide are covalently linked.

7. (As filed) The isolated receptor of claim 4, wherein the heterologous polypeptide is a T1R1 polypeptide that is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:1, 2, or 3.

8. (As filed) The isolated receptor of claim 4, wherein the heterologous polypeptide is a T1R1 polypeptide that is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:1, 2, or 3.

9. (As filed) The isolated receptor of claim 7, wherein the T1R1 polypeptide has an amino acid sequence of SEQ ID NO:1, 2, or 3.

10. (As filed) The isolated receptor of claim 4, wherein the heterologous polypeptide is a T1R2 polypeptide that is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:7, 8, or 9.

11. (As filed) The isolated receptor of claim 4, wherein the heterologous polypeptide is a T1R2 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:7, 8, or 9.

12. (As filed) The isolated receptor of claim 10, wherein the T1R2 polypeptide has an amino acid sequence of SEQ ID NO:7, 8, or 9.

13. (As filed) The isolated receptor of claim 1, wherein the receptor has G protein coupled receptor activity.

14. (As filed) The isolated receptor of claim 1, wherein the receptor specifically binds to antibodies raised against SEQ ID NO: 15, 20, 23, or 25.

15. (As filed) An isolated sweet taste receptor comprising a T1R3 polypeptide and a T1R1 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25; and wherein the T1R1 polypeptide that is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:1, 2, or 3.

16. (As filed) An isolated sweet taste receptor comprising a T1R3 polypeptide and a T1R2 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25; and wherein the T1R2 polypeptide that is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:7, 8, or 9.

17. (As filed) An antibody that specifically binds to the taste receptor claim 1.

18. (As filed) The antibody of claim 17, wherein the antibody specifically binds to a taste receptor comprising T1R1 and T1R3.

19. (As filed) The antibody of claim 18, wherein the T1R1 polypeptide and the T1R3 polypeptide are non-covalently linked.

20. (As filed) The antibody of claim 18, wherein the T1R1 polypeptide and the T1R3 polypeptide are covalently linked.

21. (As filed) The antibody of claim 17, wherein the antibody specifically binds to a taste receptor comprising T1R2 and T1R3.

22. (As filed) The antibody of claim 21, wherein the T1R2 polypeptide and the T1R3 polypeptide are non-covalently linked.

23. (As filed) The antibody of claim 21, wherein the T1R2 polypeptide and the T1R3 polypeptide are covalently linked.

24. (As filed) A method of identifying a compound that modulates sweet taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with a sweet taste receptor comprising a T1R3 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates sweet signal transduction.

25. (As filed) The method of claim 24, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25

26. (As filed) The method of claim 24, wherein the receptor comprises a T1R3 polypeptide and a heterologous polypeptide.

27. (As filed) The method of claim 25, wherein the T1R3 polypeptide and the heterologous polypeptide are non-covalently linked.

28. (As filed) The method of claim 25, wherein the heterologous polypeptide is a T1R1 polypeptide encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:1, 2, or 3.

29. (As filed) The method of claim 25, wherein the heterologous polypeptide is a T1R1 polypeptide encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:1, 2, or 3.

30. (As filed) The method of claim 25, wherein the T1R1 polypeptide has an amino acid sequence of SEQ ID NO:1, 2, or 3.

31. (As filed) The method of claim 25, wherein the heterologous polypeptide is a T1R2 polypeptide encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:7, 8, or 9.

32. (As filed) The method of claim 25, wherein the heterologous polypeptide is a T1R2 polypeptide encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:7, 8, or 9.

33. (Once Amended) The method of claim 25, wherein the T1R2 polypeptide has an amino acid sequence of SEQ ID NO:7, 8, or 9.

34. (As filed) The method of claim 24, wherein the receptor is recombinant.

35. (As filed) The method of claim 24, wherein the receptor has G protein coupled receptor activity.

36. (As filed) The method of claim 24, wherein the functional effect is measured *in vitro*.

37. (As filed) The method of claim 36, wherein the functional effect is a physical effect.

38. (As filed) The method of claim 36, wherein the receptor is linked to a solid phase.

39. (As filed) The method of claim 36, wherein the functional effect is determined by measuring binding of a compound to the receptor.

40. (As filed) The method of claim 39, wherein the functional effect is determined by measuring binding of a compound to the extracellular domain of the receptor.

41. (As filed) The method of claim 24, wherein the receptor is expressed in a cell or cell membrane.

42. (As filed) The method of claim 41, wherein the functional effect is a physical effect.

43. (As filed) The method of claim 42, wherein the functional effect is determined by measuring ligand binding to the receptor.

44. (As filed) The method of claim 43, wherein the functional effect is determined by measuring binding of a compound to the extracellular domain of the receptor.

45. (As filed) The method of claim 41, wherein the functional effect is a chemical or phenotypic effect.

46. (As filed) The method of claim 45, wherein the functional effect is determined by measuring changes in intracellular cAMP, IP3, or Ca^{2+}.

47. (As filed) The method of claim 41, wherein the cell is a mammalian cell.

48. (As filed) The method of claim 47, wherein the cell is a human cell.

49. (As filed) A method of identifying a compound that modulates sweet taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with cell expressing a sweet taste receptor comprising a T1R3 polypeptide and a T1R2 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25; and wherein the T1R2 polypeptide that is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:7, 8, or 9; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates sweet signal transduction.

50. (As filed) The method of claim 49, wherein the T1R2 polypeptide and the T1R3 polypeptide are non-covalently linked.

51. (As filed) The method of claim 49, wherein the T1R2 polypeptide and the T1R3 polypeptide are covalently linked.

52. (As filed) A method of identifying a compound that modulates sweet taste signal transduction in taste cells, the method comprising the steps of

(i) contacting the compound with cell expressing a sweet taste receptor comprising a T1R3 polypeptide and a T1R1 polypeptide, wherein the T1R3 polypeptide is encoded by a nucleotide sequence that hybridizes under highly stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:15, 20, 23, or 25; and wherein the T1R1 polypeptide that is encoded by a nucleotide sequence that hybridizes under moderately stringent hybridization conditions to a nucleotide sequence encoding an amino acid sequence of SEQ ID NO:1, 2, or 3; and

(ii) determining the functional effect of the compound upon the receptor, thereby identifying a compound that modulates sweet signal transduction.

53. (As filed) The method of claim 52, wherein the T1R1 polypeptide and the T1R3 polypeptide are non-covalently linked.

54. (As filed) The method of claim 52, wherein the T1R1 polypeptide and the T1R3 polypeptide are covalently linked.